

6271346

FIG. 1A

GAATTCTCTGGACTGAGGCTCCAGTTCTGGCCTTG
TTCAAGATCACTGGACCAGGCCGTATCTCTATGCCGAGTCTCAACCCCTCAACTGTC
ACCCCAAGGCACTTGGACGTCTGGACAGACCGAGTCCGGAGCCCCAGCACTGCC

GCTGCCACACTGCCCTGAGCCAAATGGGGAGTGAGAGGCCA TAG CTG TCT GGC

S1	S5	S10	S15
Met	Gly	Leu	Ser
ATG	GGC	CTC	CTC
216	225	234	243
Thr	Val	Pro	Asp
TCC	TCC	ACC	GTG
261	270	279	288
Val	Gly	Ile	Tyr
CTG	GAG	CTG	TTG
297	306	315	324
Gly	Ile	Tyr	Pro
CTG	GAG	GTG	CCT
342	351	360	369
Asp	Arg	Glu	Arg
GAC	AGG	GAG	AAG
387	396	405	414
Arg	Ser	Asp	Ser
GAT	AGA	GAT	AGT
423	432	441	450
Ser	Ile	Cys	Cys
AGT	AGA	TGT	TGT
468	477	486	495
Cys	Cys	Thr	Asp
TGT	TGT	GAT	CAC
495	504	513	522
Asp	Cys	Arg	Gly
GAT	GAC	AGG	Glu
558	567	531	540
Arg	Lys	Glu	Met
CGA	AAG	GAA	ATG
567	576	585	594
Gly	Gln	Val	Gly
GGT	CAG	Glu	Glu
594	603	612	621
Val	Ser	Ser	Cys
TCT	TCT	TCT	TCC
621	630	640	650
Asp	Thr	Lys	Cys
GAC	GTC	GAA	GAC
650	660	670	680
Asp	Asp	Asp	Asp
GAC	GAC	GAC	GAC
680	690	700	710
Asp	Asp	Asp	Asp
GAC	GAC	GAC	GAC
710	720	730	740
Asp	Asp	Asp	Asp
GAC	GAC	GAC	GAC
740	750	760	770
Asp	Asp	Asp	Asp
GAC	GAC	GAC	GAC
770	780	790	800
Asp	Asp	Asp	Asp
GAC	GAC	GAC	GAC
800	810	820	830
Asp	Asp	Asp	Asp
GAC	GAC	GAC	GAC
830	840	850	860
Asp	Asp	Asp	Asp
GAC	GAC	GAC	GAC
860	870	880	890
Asp	Asp	Asp	Asp
GAC	GAC	GAC	GAC
890	900	910	920
Asp	Asp	Asp	Asp
GAC	GAC	GAC	GAC
920	930	940	950
Asp	Asp	Asp	Asp
GAC	GAC	GAC	GAC
950	960	970	980
Asp	Asp	Asp	Asp
GAC	GAC	GAC	GAC
980	990	1000	1010
Asp	Asp	Asp	Asp
GAC	GAC	GAC	GAC
1010	1020	1030	1040
Asp	Asp	Asp	Asp
GAC	GAC	GAC	GAC
1040	1050	1060	1070
Asp	Asp	Asp	Asp
GAC	GAC	GAC	GAC
1070	1080	1090	1100
Asp	Asp	Asp	Asp
GAC	GAC	GAC	GAC
1100	1110	1120	1130
Asp	Asp	Asp	Asp
GAC	GAC	GAC	GAC
1130	1140	1150	1160
Asp	Asp	Asp	Asp
GAC	GAC	GAC	GAC
1160	1170	1180	1190
Asp	Asp	Asp	Asp
GAC	GAC	GAC	GAC
1190	1200	1210	1220
Asp	Asp	Asp	Asp
GAC	GAC	GAC	GAC
1220	1230	1240	1250
Asp	Asp	Asp	Asp
GAC	GAC	GAC	GAC
1250	1260	1270	1280
Asp	Asp	Asp	Asp
GAC	GAC	GAC	GAC
1280	1290	1300	1310
Asp	Asp	Asp	Asp
GAC	GAC	GAC	GAC
1310	1320	1330	1340
Asp	Asp	Asp	Asp
GAC	GAC	GAC	GAC
1340	1350	1360	1370
Asp	Asp	Asp	Asp
GAC	GAC	GAC	GAC
1370	1380	1390	1400
Asp	Asp	Asp	Asp
GAC	GAC	GAC	GAC
1400	1410	1420	1430
Asp	Asp	Asp	Asp
GAC	GAC	GAC	GAC
1430	1440	1450	1460
Asp	Asp	Asp	Asp
GAC	GAC	GAC	GAC
1460	1470	1480	1490
Asp	Asp	Asp	Asp
GAC	GAC	GAC	GAC
1490	1500	1510	1520
Asp	Asp	Asp	Asp
GAC	GAC	GAC	GAC
1520	1530	1540	1550
Asp	Asp	Asp	Asp
GAC	GAC	GAC	GAC
1550	1560	1570	1580
Asp	Asp	Asp	Asp
GAC	GAC	GAC	GAC
1580	1590	1600	1610
Asp	Asp	Asp	Asp
GAC	GAC	GAC	GAC
1610	1620	1630	1640
Asp	Asp	Asp	Asp
GAC	GAC	GAC	GAC
1640	1650	1660	1670
Asp	Asp	Asp	Asp
GAC	GAC	GAC	GAC
1670	1680	1690	1700
Asp	Asp	Asp	Asp
GAC	GAC	GAC	GAC
1700	1710	1720	1730
Asp	Asp	Asp	Asp
GAC	GAC	GAC	GAC
1730	1740	1750	1760
Asp	Asp	Asp	Asp
GAC	GAC	GAC	GAC
1760	1770	1780	1790
Asp	Asp	Asp	Asp
GAC	GAC	GAC	GAC
1790	1800	1810	1820
Asp	Asp	Asp	Asp
GAC	GAC	GAC	GAC
1820	1830	1840	1850
Asp	Asp	Asp	Asp
GAC	GAC	GAC	GAC
1850	1860	1870	1880
Asp	Asp	Asp	Asp
GAC	GAC	GAC	GAC
1880	1890	1900	1910
Asp	Asp	Asp	Asp
GAC	GAC	GAC	GAC
1910	1920	1930	1940
Asp	Asp	Asp	Asp
GAC	GAC	GAC	GAC
1940	1950	1960	1970
Asp	Asp	Asp	Asp
GAC	GAC	GAC	GAC
1970	1980	1990	2000
Asp	Asp	Asp	Asp
GAC	GAC	GAC	GAC
2000	2010	2020	2030
Asp	Asp	Asp	Asp
GAC	GAC	GAC	GAC
2030	2040	2050	2060
Asp	Asp	Asp	Asp
GAC	GAC	GAC	GAC
2060	2070	2080	2090
Asp	Asp	Asp	Asp
GAC	GAC	GAC	GAC
2090	2100	2110	2120
Asp	Asp	Asp	Asp
GAC	GAC	GAC	GAC
2120	2130	2140	2150
Asp	Asp	Asp	Asp
GAC	GAC	GAC	GAC
2150	2160	2170	2180
Asp	Asp	Asp	Asp
GAC	GAC	GAC	GAC
2180	2190	2200	2210
Asp	Asp	Asp	Asp
GAC	GAC	GAC	GAC
2210	2220	2230	2240
Asp	Asp	Asp	Asp
GAC	GAC	GAC	GAC
2240	2250	2260	2270
Asp	Asp	Asp	Asp
GAC	GAC	GAC	GAC
2270	2280	2290	2300
Asp	Asp	Asp	Asp
GAC	GAC	GAC	GAC
2300	2310	2320	2330
Asp	Asp	Asp	Asp
GAC	GAC	GAC	GAC
2330	2340	2350	2360
Asp	Asp	Asp	Asp
GAC	GAC	GAC	GAC
2360	2370	2380	2390
Asp	Asp	Asp	Asp
GAC	GAC	GAC	GAC
2390	2400	2410	2420
Asp	Asp	Asp	Asp
GAC	GAC	GAC	GAC
2420	2430	2440	2450
Asp	Asp	Asp	Asp
GAC	GAC	GAC	GAC
2450	2460	2470	2480
Asp	Asp	Asp	Asp
GAC	GAC	GAC	GAC
2480	2490	2500	2510
Asp	Asp	Asp	Asp
GAC	GAC	GAC	GAC
2510	2520	2530	2540
Asp	Asp	Asp	Asp
GAC	GAC	GAC	GAC
2540	2550	2560	2570
Asp	Asp	Asp	Asp
GAC	GAC	GAC	GAC
2570	2580	2590	2600
Asp	Asp	Asp	Asp
GAC	GAC	GAC	GAC
2600	2610	2620	2630
Asp	Asp	Asp	Asp
GAC	GAC	GAC	GAC
2630	2640	2650	2660
Asp	Asp	Asp	Asp
GAC	GAC	GAC	GAC
2660	2670	2680	2690
Asp	Asp	Asp	Asp
GAC	GAC	GAC	GAC
2690	2700	2710	2720
Asp	Asp	Asp	Asp
GAC	GAC	GAC	GAC
2720	2730	2740	2750
Asp	Asp	Asp	Asp
GAC	GAC	GAC	GAC
2750	2760	2770	2780
Asp	Asp	Asp	Asp
GAC	GAC	GAC	GAC
2780	2790	2800	2810
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GAC	GAC	GAC	GAC
2810	2820	2830	2840
Asp	Asp	Asp	Asp
GAC	GAC	GAC	GAC
2840	2850	2860	2870
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GAC	GAC	GAC	GAC
2870	2880	2890	2900
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GAC	GAC	GAC	GAC
2900	2910	2920	2930
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GAC	GAC	GAC	GAC
2930	2940	2950	2960
Asp	Asp	Asp	Asp
GAC	GAC	GAC	GAC
2960	2970	2980	2990
Asp	Asp	Asp	Asp
GAC	GAC	GAC	GAC
2990	3000	3010	3020
Asp	Asp	Asp	Asp
GAC	GAC	GAC	GAC
3020	3030	3040	3050
Asp	Asp	Asp	Asp
GAC	GAC	GAC	GAC
3050	3060	3070	3080
Asp	Asp	Asp	Asp
GAC	GAC	GAC	GAC
3080	3090	3100	3110
Asp	Asp	Asp	Asp
GAC	GAC	GAC	GAC
3110	3120	3130	3140
Asp	Asp	Asp	Asp
GAC	GAC	GAC	GAC
3140	3150	3160	3170
Asp	Asp	Asp	Asp
GAC	GAC	GAC	GAC
3170	3180	3190	3200
Asp	Asp	Asp	Asp
GAC	GAC	GAC	GAC
3200	3210	3220	3230
Asp	Asp	Asp	Asp
GAC	GAC	GAC	GAC
3230	3240	3250	3260
Asp	Asp	Asp	Asp
GAC	GAC	GAC	GAC
3260	3270	3280	3290
Asp	Asp	Asp	Asp
GAC	GAC	GAC	GAC
3290	3300	3310	3320
Asp	Asp	Asp	Asp
GAC	GAC	GAC	GAC
3320	3330	3340	3350
Asp	Asp	Asp	Asp
GAC	GAC	GAC	GAC
3350	3360	3370	3380
Asp	Asp	Asp	Asp
GAC	GAC	GAC	GAC
3380	3390	3400	3410
Asp	Asp	Asp	Asp
GAC	GAC	GAC	GAC
3410	3420	3430	3440
Asp	Asp	Asp	Asp
GAC	GAC	GAC	GAC
3440	3450	3460	3470
Asp	Asp	Asp	Asp
GAC	GAC	GAC	GAC
3470	3480	3490	3500
Asp	Asp	Asp	Asp
GAC	GAC	GAC	GAC
3500	3510	3520	3530
Asp	Asp	Asp	Asp
GAC	GAC	GAC	GAC
3530	3540	3550	3560
Asp	Asp	Asp	Asp
GAC	GAC	GAC	GAC
3560	3570	3580	3590
Asp	Asp	Asp	Asp
GAC	GAC	GAC	GAC
3590	3600	3610	3620
Asp	Asp	Asp	Asp
GAC	GAC	GAC	GAC
3620	3630	3640	3650
Asp	Asp	Asp	Asp
GAC	GAC	GAC	

FIG. 1B

95	100	105
Arg Asp Thr Val Cys Gly Cys Arg Lys Asn Gln Tyr Arg His Tyr		
CGG GAC ACC GTG TGT GGC TGC AGG AAG AAC CAG TAC CGG CAT TAT		
576	585	594
		603
		612
110	115	120
Trp Ser Glu Asn Leu Phe Gln Cys Phe Asn Cys Ser Leu Cys Leu		
TGG AGT GAA AAC CTT TTC CAG TGC TTC AAT TGC AGC CTC TGC CTC		
621	630	639
		648
		657
125	130	135
Asn Gly Thr Val His Leu Ser Cys Gln Glu Lys Gln Asn Thr Val		
AAT GGG ACC GTG CAC CTC TCC TGC CAG GAG AAA CAG AAC ACC GTG		
666	675	684
		693
		702
140	145	150
Cys Thr Cys His Ala Gly Phe Phe Leu Arg Glu Asn Glu Cys Val		
TGC ACC TGC CAT GCA GGT TTC TTT CTA AGA GAA AAC GAG TGT GTC		
711	720	729
		738
		747
155	160	165
Ser Cys Ser Asn Cys Lys Lys Ser Leu Glu Cys Thr Lys Leu Cys		
TCC TGT AGT AAC TGT AAG AAA AGC CTG GAG TGC ACG AAG TTG TGC		
756	765	774
		783
		792
170	175	180
Leu Pro Gln Ile Glu Asn Val Lys Gly Thr Glu Asp Ser Gly Thr		
CTA CCC CAG ATT GAG AAT GTT AAG GGC ACT GAG GAC TCA GGC ACC		
801	810	819
		828
		837
185	190	195
Thr Val Leu Leu Pro Leu Val Ile Phe Phe Gly Leu Cys Leu Leu		
ACA GTG CTG TTG CCC CTG GTC ATT TTC TTT GGT CTT TGC CTT TTA		
846	855	864
		873
		882
200	205	210
Ser Leu Leu Phe Ile Gly Leu Met Tyr Arg Tyr Gln Arg Trp Lys		
TCC CTC CTC TTC ATT GGT TTA ATG TAT CGC TAC CAA CGG TGG AAG		
891	900	909
		918
		927
215	220	225
Ser Lys Leu Tyr Ser Ile Val Cys Gly Lys Ser Thr Pro Glu Lys		
TCC AAG CTC TAC TCC ATT GTT TGT GGG AAA TCG ACA CCT GAA AAA		
936	945	954
		963
		972
230	235	240
Glu Gly Glu Leu Glu Gly Thr Thr Thr Lys Pro Leu Ala Pro Asn		
GAG GGG GAG CTT GAA GGA ACT ACT ACT AAG CCC CTG GCC CCA AAC		
981	990	999
		1008
		1017

FIG. 1C

245	250	255
Pro Ser Phe Ser Pro Thr Pro Gly Phe Thr Pro Thr Leu Gly Phe		
CCA AGC TTC AGT CCC ACT CCA GGC TTC ACC CCC ACC CTG GGC TTC		
1026	1035	1044
1053	1062	
260	265	270
Ser Pro Val Pro Ser Ser Thr Phe Thr Ser Ser Ser Thr Tyr Thr		
AGT CCC GTG CCC AGT TCC ACC TTC ACC TCC AGC TCC ACC ACC TAT ACC		
1071	1080	1089
1098	1107	
275	280	285
Pro Gly Asp Cys Pro Asn Phe Ala Ala Pro Arg Arg Glu Val Ala		
CCC GGT GAC TGT CCC AAC TTT GCG GCT CCC CGC AGA GAG GTG GCA		
1116	1125	1134
1143	1152	
290	295	300
Pro Pro Tyr Gln Gly Ala Asp Pro Ile Leu Ala Thr Ala Leu Ala		
CCA CCC TAT CAG GGG GCT GAC CCC ATC CTT GCG ACA GCC CTC GCC		
1161	1170	1179
1188	1197	
305	310	315
Ser Asp Pro Ile Pro Asn Pro Leu Gln Lys Trp Glu Asp Ser Ala		
TCC GAC CCC ATC CCC AAC CCC CTT CAG AAG TGG GAG GAC AGC GCC		
1206	1215	1224
1233	1242	
320	325	330
His Lys Pro Gln Ser Leu Asp Thr Asp Asp Pro Ala Thr Leu Tyr		
CAC AAG CCA CAG AGC CTA GAC ACT GAT GAC CCC GCG ACG CTG TAC		
1251	1260	1269
1278	1287	
335	340	
Ala Val Val Glu Asn Val Pro Pro Leu Arg Trp		
GCC GTG GTG GAG AAC GTG CCC CCG TTG CGC TGG AA <u>GGAATTC</u>		
1296	1305	1314
1323	1332	

FIG. 2

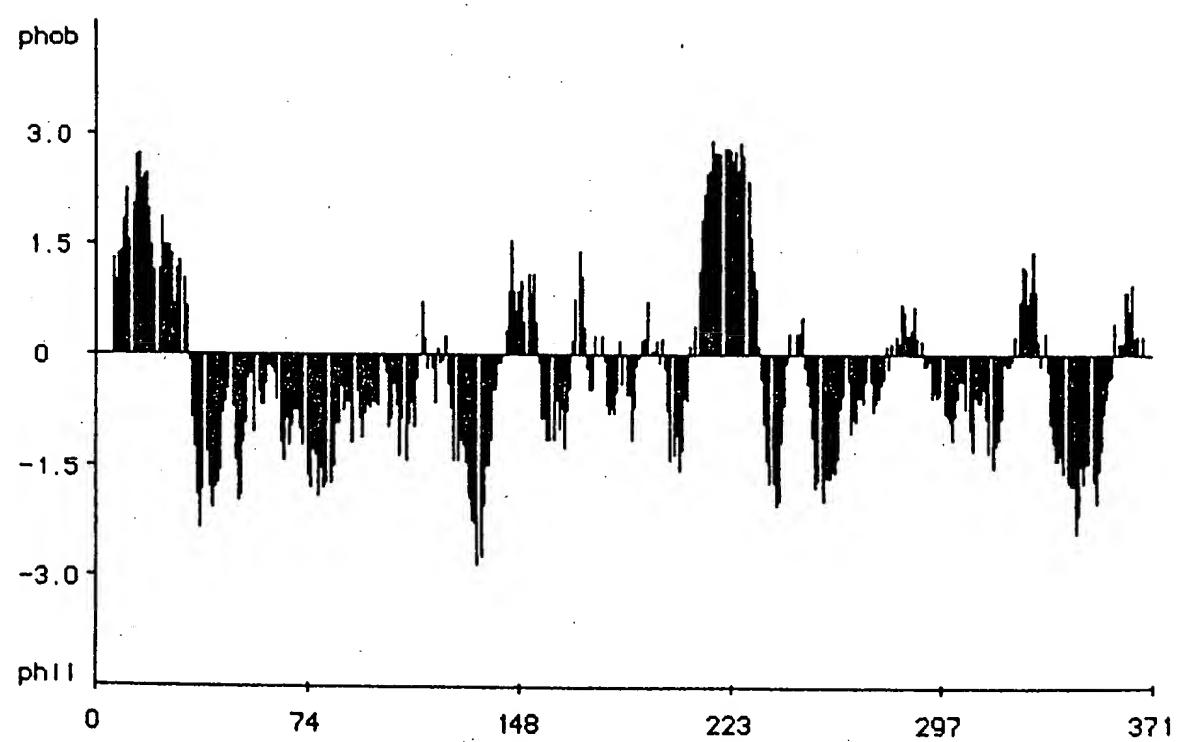


FIG. 3A

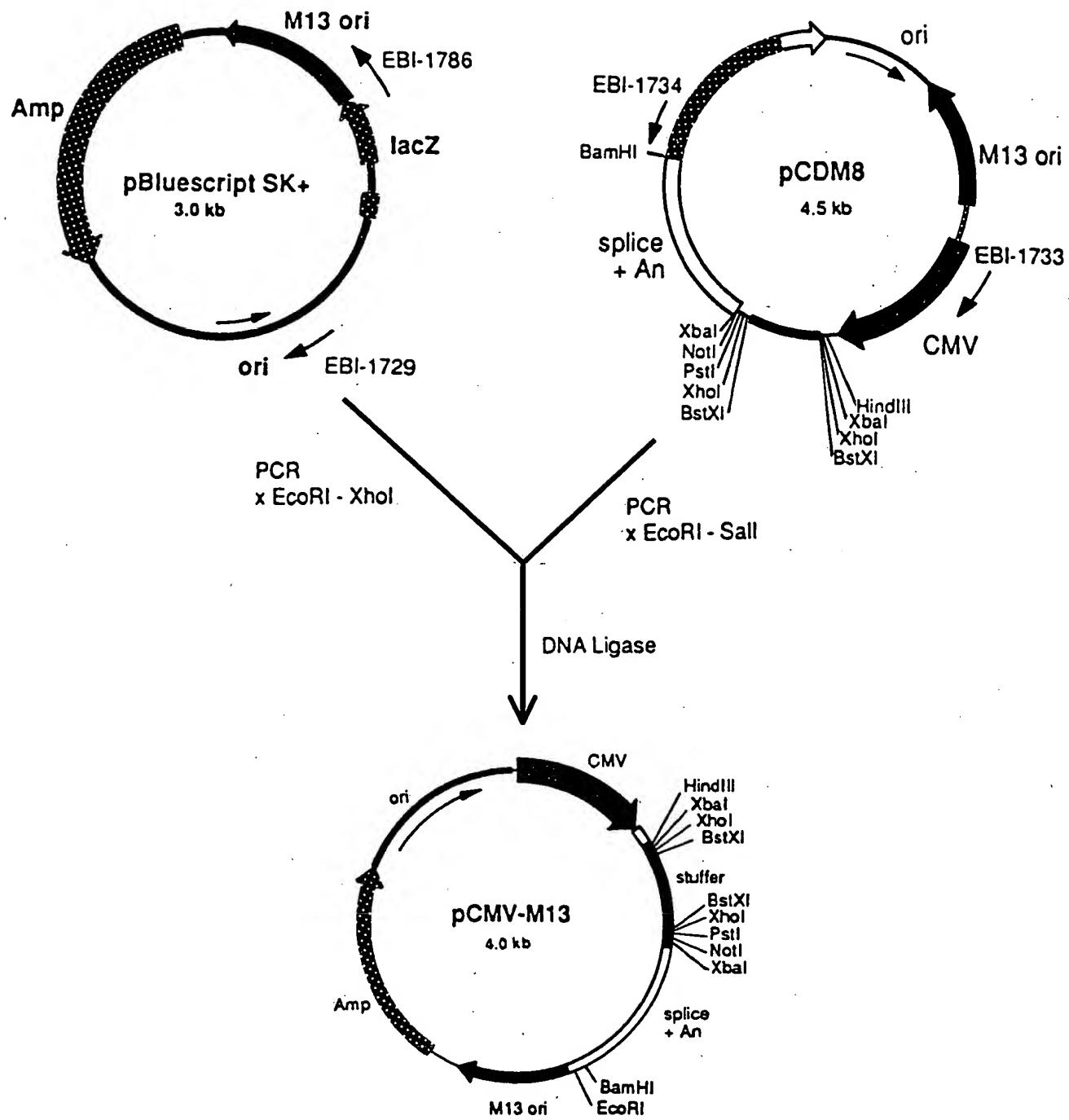


FIG. 3B

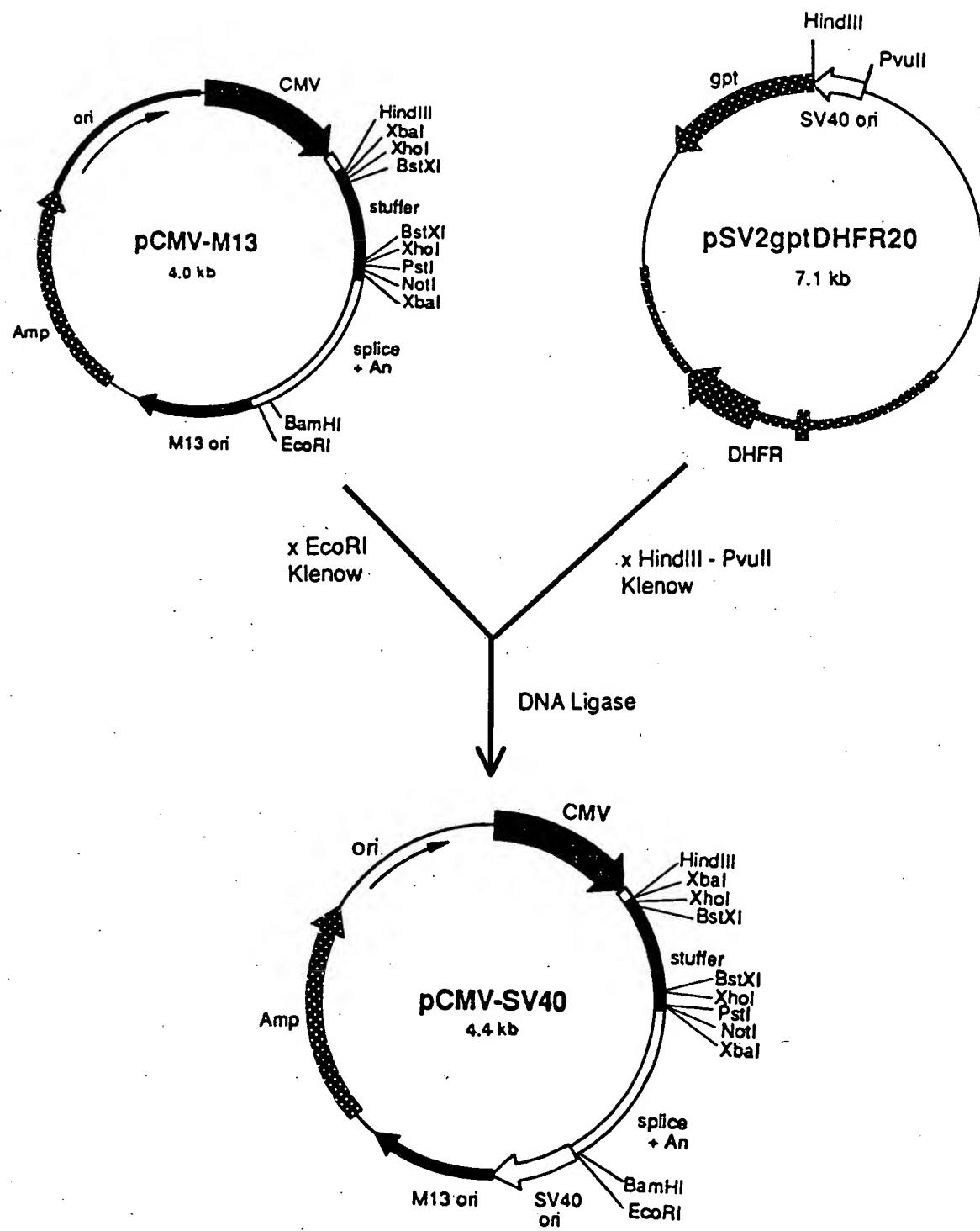


FIG. 4A

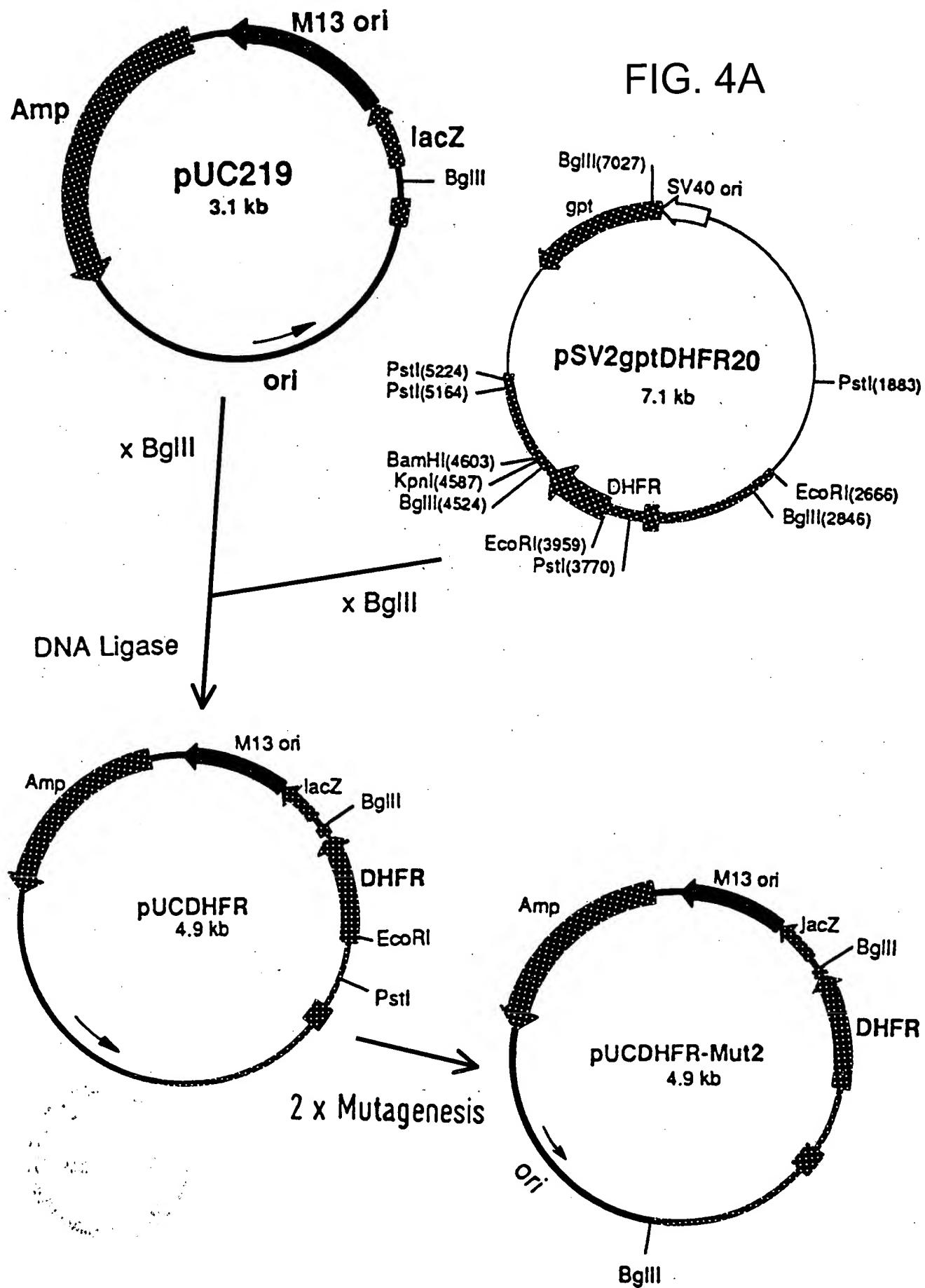


FIG. 4B

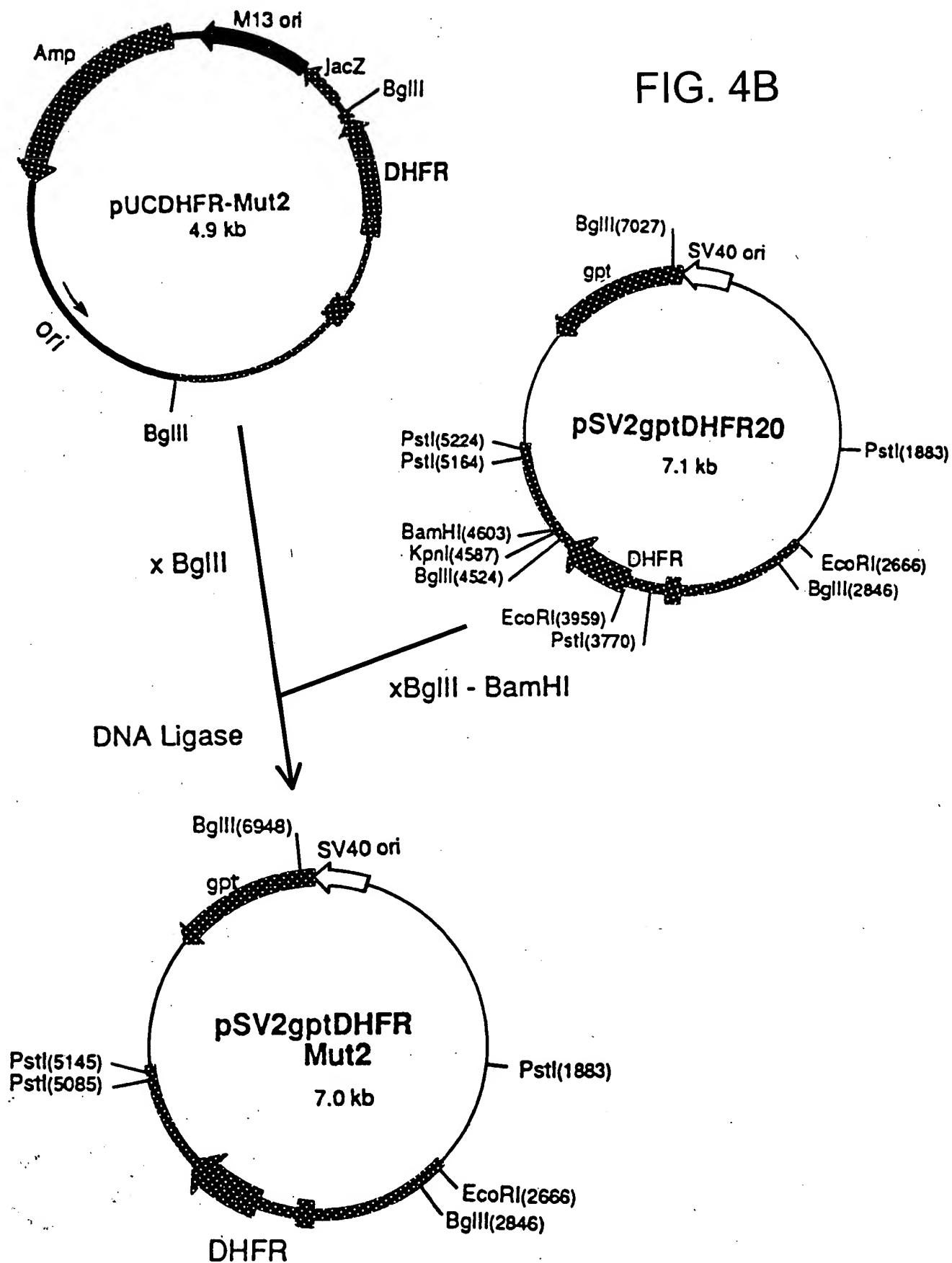


FIG. 5A

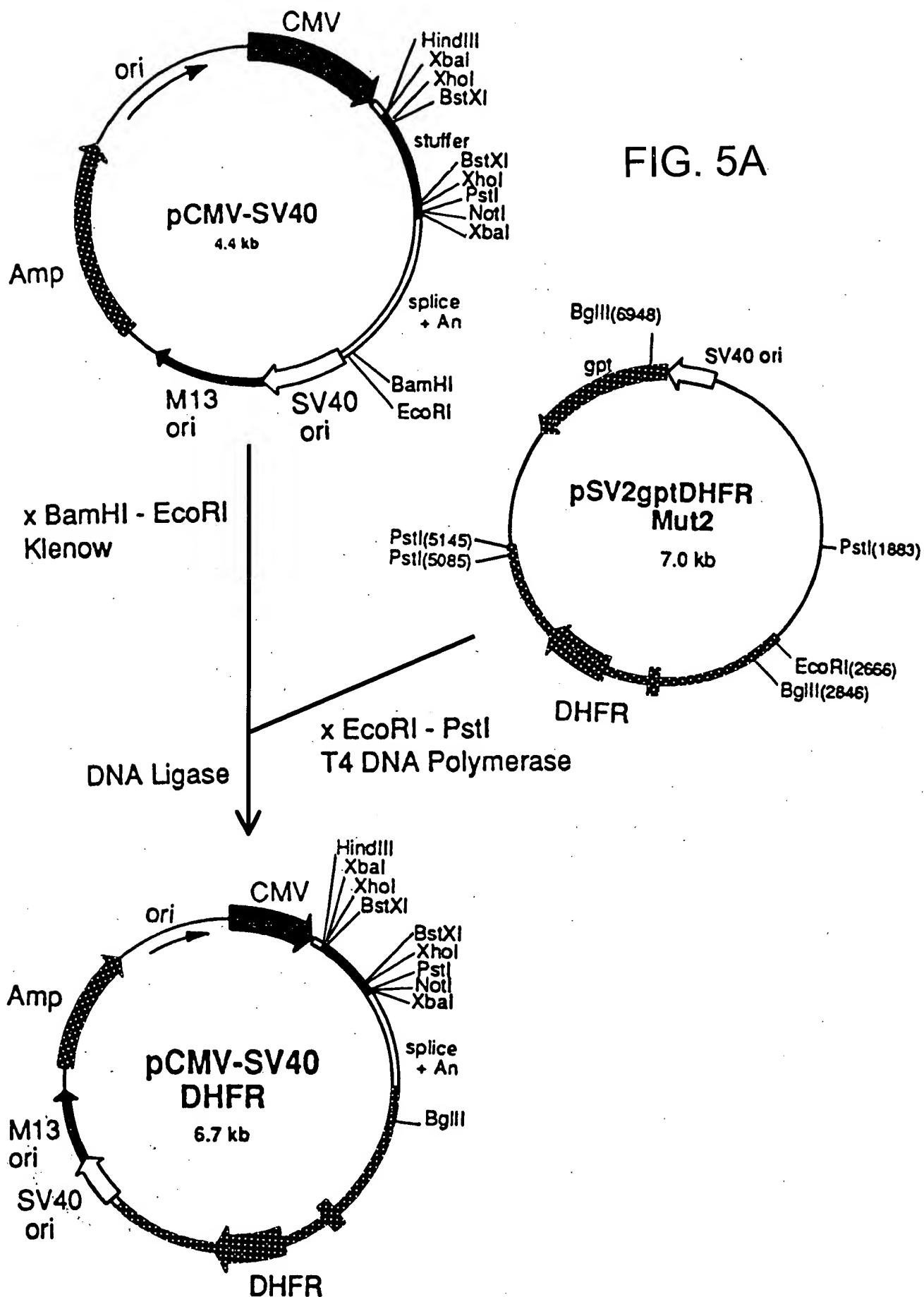


FIG. 5B

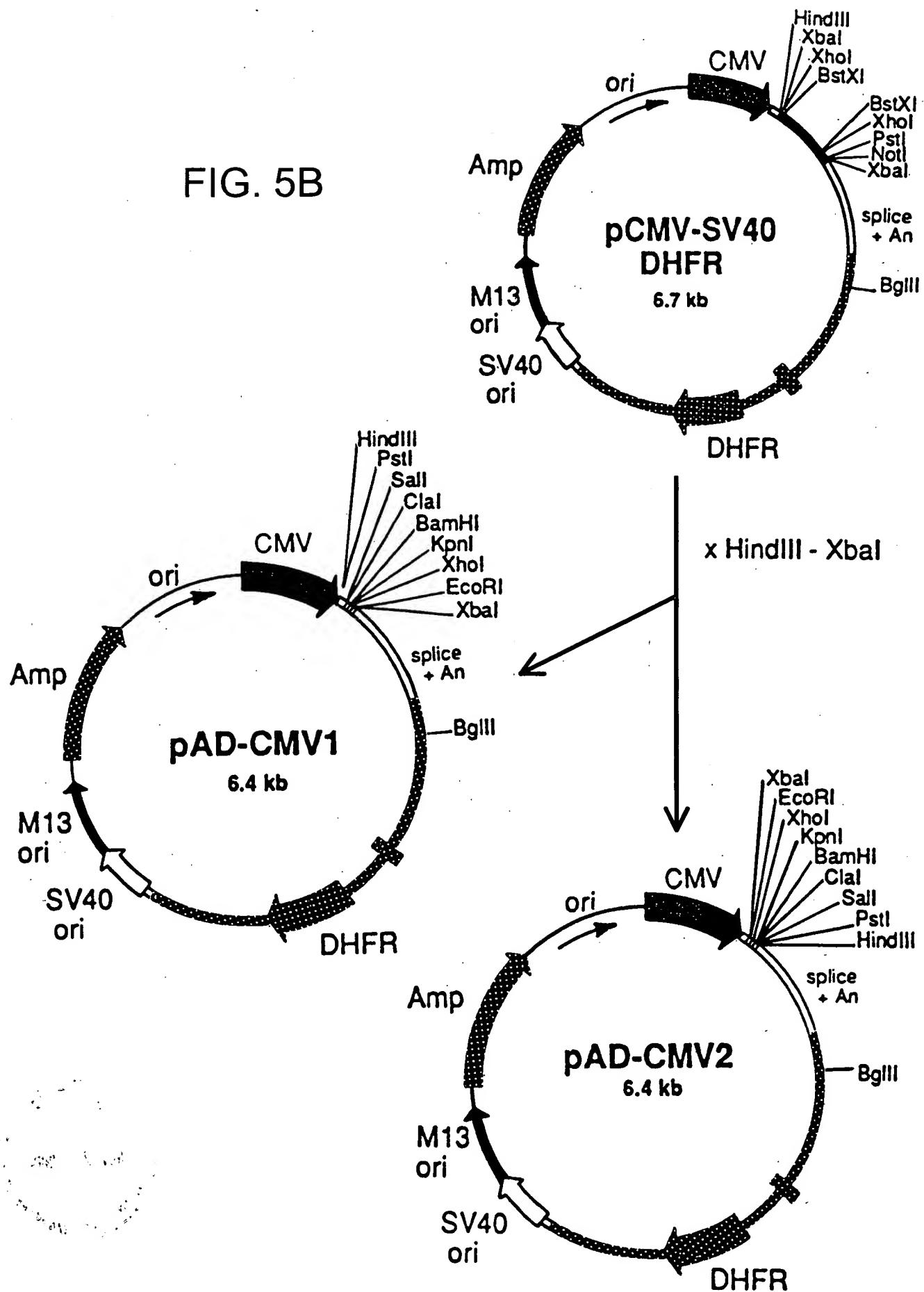


FIG. 6A

pAD-CMV1 : 6414 bp

TCGACATTGA TTATTGACTA GTTATTAATA GTAATCAATT ACGGGGTCA	60
CCCATATATG GAGTTCCGCG TTACATAACT TACGGTAAAT GGCCCGCCTG GCTGACCGCC	120
CAACGACCCC CGCCCATTGA CGTCAATAAT GACGTATGTT CCCATAGTAA CGCCAATAGG	180
GACTTTCCAT TGACGTCAAT GGGTGGAGTA TTTACGGTAA ACTGCCCACT TGGCAGTACA	240
TCAAGTGTAT CATATGCCAA GTACGCCCCC TATTGACGTC AATGACGGTA AATGGCCCGC	300
CTGGCATTAT GCCCAGTACA TGACCTTATG GGACTTCCT ACTTGGCAGT ACATCTACGT	360
ATTAGTCATC GCTATTACCA TGGTGATGCG GTTTGCGAG TACATCAATG GCGTGGATA	420
GC GGTTTGAC TCACGGGAT TTCCAAGTCT CCACCCATT GACGTCAATG GGAGTTGTT	480
TTGGCACCAA AATCAACGGG ACTTCCAAA ATGTCGTAAC AACTCCGCC CATTGACGCA	540
AATGGCGGT AGGCGTGTAC GGTGGGAGGT CTATATAAGC AGAGCTCTCT GGCTAACTAG	600
AGAACCCACT GCTTAACTGG CTTATCGAAA TTAATACGAC TCACTATAGG GAGACCCAAG	660
CTTCTGCAGG TCGACATCGA TGGATCCGGT ACCTCGAGCG CGAATTCTCT AGAGGATCTT	720
TGTGAAGGAA CCTTACTTCT GTGGTGTGAC ATAATTGGAC AACTACCTA CAGAGATTTA	780
AAGCTCTAAG GTAAATATAA AATTTTAAG TGTATAATGT GTTAAACTAC TGATTCTAAT	840
TGTTTGTGTA TTTAGATTC CAACCTATGG AACTGATGAA TGGGAGCAGT GGTGGAATGC	900
CTTTAATGAG GAAAACCTGT TTTGCTCAGA AGAAATGCCA TCTAGTGATG ATGAGGCTAC	960
TGCTGACTCT CAACATTCTA CTCCTCCAAA AAAGAAGAGA AAGGTAGAAG ACCCCAAGGA	1020
CTTCCTTCA GAATTGCTAA GTTTTGAG TCATGCTGTG TTTAGTAATA GAACTCTTGC	1080
TTGCTTGCT ATTTACACCA CAAAGGAAAA AGCTGCACTG CTATACAAGA AAATTATGGA	1140
AAAATATTG ATGTATAGTG CCTTGACTAG AGATCATAAT CAGCCATACC ACATTTGTAG	1200
AGGTTTACT TGCTTAAAA AACCTCCAC ACCTCCCCCT GAACCTGAAA CATAAAATGA	1260
ATGCAATTGT TGTTGTTAAC TTGTTATTG CAGCTTATAA TGGTTACAAA TAAAGCAATA	1320
GCATCACAAA TTTCACAAAT AAAGCATTCTT TTCACTGCA TTCTAGTTGT GGTTGTCCA	1380
AACTCATCAA TGTATCTTAT CATGTCTGGA TCAATTCTGA GAAACTAGCC TTAAAGACAG	1440

FIG. 6B

ACAGCTTGT TCTAGTCAGC CAGGCAAGCA TATGTAATAA AAGTTCTCA GGGAACTGAG	1500
GTTAAAAGAT GTATCCTGGA CCTGCCAGAC CTGGCCATT ACAGTAAACAG AAGATTCCGC	1560
CTCAAGTTCC GGTTAACAAAC AGGAGGCAAC GAGATCTAA ATCTATTACT TCTAATCGGG	1620
TAATTAAAAC CTTTCAACTA AAACACGGAC CCACGGATGT CACCCACTTT TCCTTCCCCG	1680
GCTCCGCCCT TCTCAGTACT CCCCACCATT AGGCTCGCTA CTCCACCTCC ACTTCCGGC	1740
GCGACACCCA CGTGCCTCT CCCACCCGAC GCTAACCCCG CCCCTGCCCG TCTGACCCCG	1800
CCCACCAACCT GGCCCCGCC CGTTGAGGAC AGAAGAAACC CCGGGCAGCC GCAGCCAAGG	1860
CGGACGGGTA GACGCTGGGG GCGCTGAGGA GTCGTCTCT ACCTTCTCTG CTGGCTCGGT	1920
GGGGGACGCG GTGGATCTCA GGCTTCCGGA AGACTGGAAG AACCGGCTCA GAACCGCTTG	1980
TCTCCGCGGG GCTTGGCGG CGGAAGAATG GCCGCTAGAC GCGGACTTGG TGCGAGGCAT	2040
CGCAGGATGC AGAAGAGCAA GCCCGCCGGG AGCGCGCGC TGTACTACCC CGCGCCTGGA	2100
CGGGCCACGC CGGACTGGGC GGGGCCGGCC TGGTGGAGGC GGAGTCTGAC CTCGTGGAGG	2160
CGGGGCCTCT GATGTTAAA TAGGATGCTA GGCTTGTGA GGCGTGGCCT CCGATTACACA	2220
AGTGGGAAGC AGCGCCGGGC GACTGCAATT TCGCGCCAAA CTTGGGGAA GCACAGCGTA	2280
CAGGCTGCCT AGGTGATCGC TGCTGCTGTC ATGGTTCGAC CGCTGAAC TG CATCGTCGCC	2340
GTGTCCCAGA ATATGGGCAT CGGCAAGAAC GGAGACCTTC CCTGGCCAAT GCTCAGGTAC	2400
TGGCTGGATT GGGTTAGGGA AACCGAGGCG GTTCGCTGAA TCGGGTCGAG CACTTGGCGG	2460
AGACGCGCGG GCCAACTACT TAGGGACAGT CATGAGGGGT AGGCCCCCG GCTGCTGCC	2520
TTGCCCATGC CCGCGGTGAT CCCCATGCTG TGCCAGCCTT TGCCAGAGG CGCTCTAGCT	2580
GGGAGCAAAG TCCGGTCACT GGGCAGCACC ACCCCCCGGA CTTGCATGGG TAGCCGCTGA	2640
GATGGAGCCT GAGCACACGT GACAGGGTCC CTGTTAACGC AGTGTTCCTC TAACTTCAG	2700
GAACGAGTTC AAGTACTTCC AAAGAATGAC CACCACCTCC TCAGTGGAAAG GTAAACAGAA	2760
CCTGGTGATT ATGGGCCGGGA AAACCTGGTT CTCCATTCTT GAGAAGAAC GACCTTAAA	2820
GGACAGAATT AATATAGTTC TCAGTAGAGA GCTCAAGGAA CCACCACAAG GAGCTCATT	2880
TCTTGCCAAA AGTCTGGACC ATGCCTTAAA ACTTATTGAA CAACCAGAGT TAGCAGATAA	2940
AGTGGACATG GTTGGATAG TTGGAGGCAG TTCCGTTAC AAGGAAGCCA TGAATCAGCC	3000

FIG. 6C

AGGCCATCTC AGACTCTTG TGACAAGGAT CATGCAGGAA TTTGAAAGTG ACACGTTCTT	3060
CCCAGAAATT GATTGGAGA AATATAAACT TCTCCCAGAG TACCCAGGGG TCCCTTCTGA	3120
AGTCCAGGAG GAAAAAGGCA TCAAGTATAA ATTTGAAGTC TATGAGAAGA AAGGCTAAC	3180
GAAAGATACT TGCTGATTGA CTTCAAGTTC TACTGCTTC CTCCTAAAT TATGCATT	3240
TACAAGACCA TGGGACTTGT GTTGGCTTA GATCCTGTGC ATCCTGGCA ACTGTTGTAC	3300
TCTAAGCCAC TCCCCAAAGT CATGCCAG CCCCTGTATA ATTCTAAACA ATTAGAATT	3360
TTTCATTTC CATTAGTCTA ACCAGGTTAT ATTAAATATA CTTAAGAAA CACCATTGC	3420
CATAAAAGTTC TCAATGCCCT TCCCAGCAG CCTCAAGTGG CTCCCCAGCA GATGCATAGG	3480
GTAGTGTGTG TACAAGAGAC CCCAAAGACA TAGAGCCCT GAGAGCATGA GCTGATATGG	3540
GGGCTCATAG AGATAGGAGC TAGATGAATA AGTACAAAGG GCAGAAATGG GTTTAACCA	3600
GCAGAGCTAG AACTCAGACT TTAAAGAAA TTAGATCAA GTAGAGACTG AATTATTCTG	3660
CACATCAGAC TCTGAGCAGA GTTCTGTTCA CTCAGACAGA AAATGGTAA ATTGAGAGCT	3720
GGCTCCATTG TGCTCCTAG AGATGGGAGC AGGTGGAGGA TTATATAAGG TCTGGAACAT	3780
TTAACTTCTC CGTTTCTCAT CTTCAAGGG ATACTACAAT TCTGTGGAAT	3840
GTGTGTCAGT TAGGGTGTGG AAAGTCCCCA GGCTCCCCAG CAGGCAGAAG TATGCAAAGC	3900
ATGCATCTCA ATTAGTCAGC AACCAAGGTGT GGAAAGTCCC CAGGCTCCCC AGCAGGCAGA	3960
AGTATGCAA GCATGCATCT CAATTAGTCA GCAACCATAG TCCCGCCCCC AACTCCGCC	4020
ATCCCGCCCC TAACTCCGCC CAGTTCCGCC CATTCTCCGC CCCATGGCTG ACTAATTTT	4080
TTTATTTATG CAGAGGCCGA GGCGCCTCTG AGCTATTCCA GAAGTAGTGA GGAGGCTTT	4140
TTGGAGGCCT AGGCTTTGC AAAAAAGCTA ATTCAAGCCTG AATGGCGAAT GGGACGCGCC	4200
CTGTAGCGGC GCATTAAGCG CGGCGGGTGT GGTGGTTACG CGCAGCGTGA CCGCTACACT	4260
TGCCAGCGCC CTAGCGCCCC CTCCTTTCGC TTTCTCCCT TCCTTCTCG CCACGTTCGC	4320
CGGCTTCCC CGTCAAGCTC TAAATCGGGG GCTCCCTTA GGGTTCCGAT TTAGTGCTT	4380
ACGGCACCTC GACCCAAAA ACTTGATTAG GGTGATGGTT CACGTAGTGG GCCATCGCCC	4440
TGATAGACGG TTTTCGCC TTTGACGTTG GAGTCCACGT TCTTTAATAG TGGACTCTT	4500
TTCCAAACTG GAACAACACT CAACCCTATC TCGGTCTATT CTTTGATTT ATAAGGGATT	4560

FIG. 6D

TTGCCGATTT CGGCCTATTG GTTAAAAAT GAGCTGATT AACAAAATT TAACGCGAAT	4620
TTTAACAAA TATTAACGTT TACAATTCA GGTGGCACTT TTCGGGAAA TGTGCGCGA	4680
ACCCCTATT GTTTATTTT CTAAATACAT TCAAATATGT ATCCGCTCAT GAGACAATAA	4740
CCCTGATAAA TGCTTCATA ATATTGAAA AGGAAGAGTA TGAGTATTCA ACATTTCCGT	4800
GTCGCCCTA TTCCCTTTT TGCGGCATT TGCGCTCCTG TTTTGCTCA CCCAGAAACG	4860
CTGGTGAAG TAAAAGATGC TGAAGATCAG TTGGGTGCAC GAGTGGTTA CATCGAACTG	4920
GATCTCAACA GCGGTAAGAT CCTTGAGAGT TTTCGCCCCG AAGAACGTTT TCCAATGATG	4980
AGCACTTTA AAGTTCTGCT ATGTGGCGCG GTATTATCCC GTATTGACGC CGGGCAAGAG	5040
CAACTCGGTC GCCGCATACA CTATTCTCAG AATGACTTGG TTGAGTACTC ACCAGTCACA	5100
GAAAAGCATC TTACGGATGG CATGACAGTA AGAGAATTAT GCAGTGCTGC CATAACCATG	5160
AGTGATAACA CTGCGGCCAA CTTACTCTG ACAACGATCG GAGGACCGAA GGAGCTAAC	5220
GCTTTTTGC ACAACATGGG GGATCATGTA ACTCGCCTG ATCGTTGGGAA ACCGGAGCTG	5280
AATGAAGCCA TACCAAACGA CGAGCGTGAC ACCACGATGC CTGTAGCAAT GGCAACAAACG	5340
TTGCGCAAAC TATTAACTGG CGAACTACTT ACTCTAGCTT CCCGGCAACA ATTAATAGAC	5400
TGGATGGAGG' CGGATAAAAGT TGCAGGACCA CTTCTGCCT CGGCCCTTCC GGCTGGCTGG	5460
TTTATTGCTG ATAAATCTGG AGCCGGTGAG CGTGGGTCTC GCGGTATCAT TGCAGCACTG	5520
GGGCCAGATG GTAAGCCCTC CCGTATCGTA GTTATCTACA CGACGGGGAG TCAGGCAACT	5580
ATGGATGAAC GAAATAGACA GATCGCTGAG ATAGGTGCCT CACTGATTAA GCATTGGTAA	5640
CTGTCAGACC AAGTTTACTC ATATATACTT TAGATTGATT TAAAACCTCA TTTTAATT	5700
AAAAGGATCT AGGTGAAGAT CCTTTTGAT AATCTCATGA CCAAAATCCC TTAACGTGAG	5760
TTTCGTTCC ACTGAGCGTC AGACCCCGTA GAAAAGATCA AAGGATCTTC TTGAGATCCT	5820
TTTTTCTGC GCGTAATCTG CTGCTTGCAA ACAAAAAAAC CACCGCTACC AGCGGTGGTT	5880
TGTTTGCCGG ATCAAGAGCT ACCAACTCTT TTTCCGAAGG TAACTGGCTT CAGCAGAGCG	5940
CAGATACCAA ATACTGTCCT TCTAGTGTAG CCGTAGTTAG GCCACCACCT CAAGAACTCT	6000
GTAGCACCAGC CTACATACCT CGCTCTGCTA ATCCTGTTAC CAGTGGCTGC TGCCAGTGGC	6060
GATAAGTCGT GTCTTACCGG GTTGGACTCA AGACGATAGT TACCGGATAA GGCGCAGCGG	6120

FIG. 6E

TCGGGCTGAA CGGGGGGTTTC GTGCACACAG CCCAGCTTGG AGCGAACGAC CTACACCGAA 6180
CTGAGATACC TACAGCGTGA GCATTGAGAA AGCGCCACGC TTCCCGAAGG GAGAAAGGCG 6240
GACAGGTATC CGGTAAGCGG CAGGGTCGGA ACAGGAGAGC GCACGAGGGA GCTTCCAGGG 6300
GGAAACGCCT GGTATCTTTA TAGTCCTGTC GGGTTTCGCC ACCTCTGACT TGAGCGTCGA 6360
TTTTGTGAT GCTCGTCAGG GGGCGGGAGC CTATGGAAAA ACGCCAGCAA CGCC

FIG. 7A

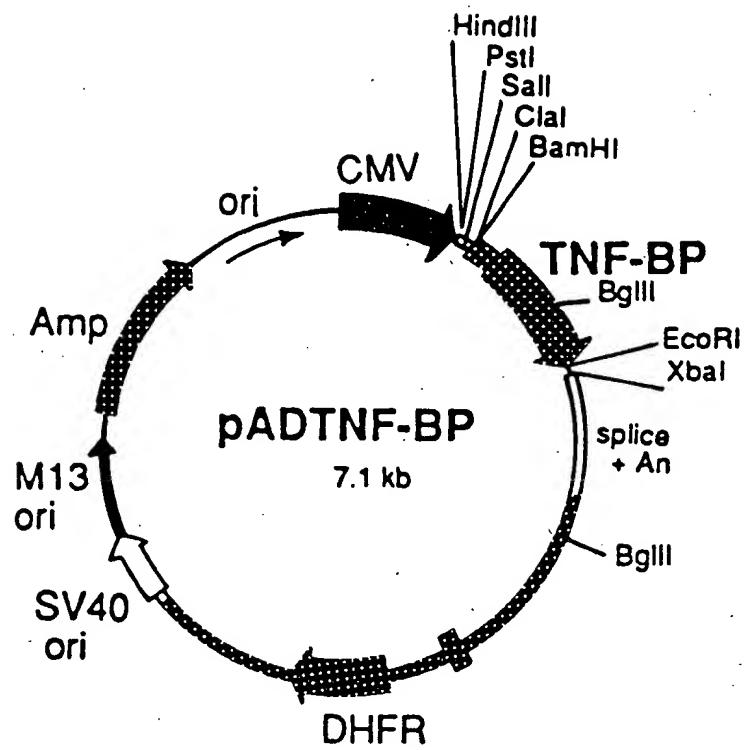


FIG. 7B

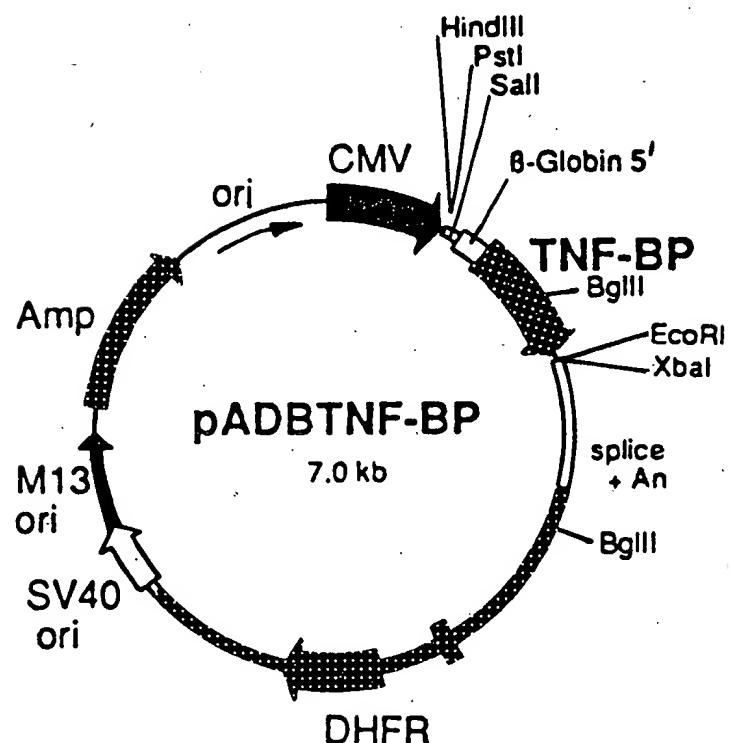


FIG. 7C

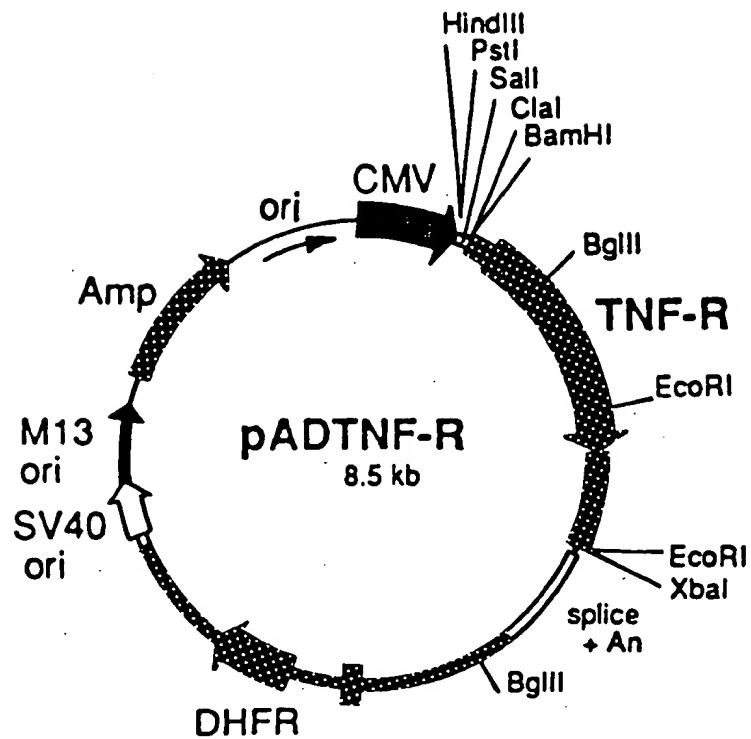


FIG. 7D

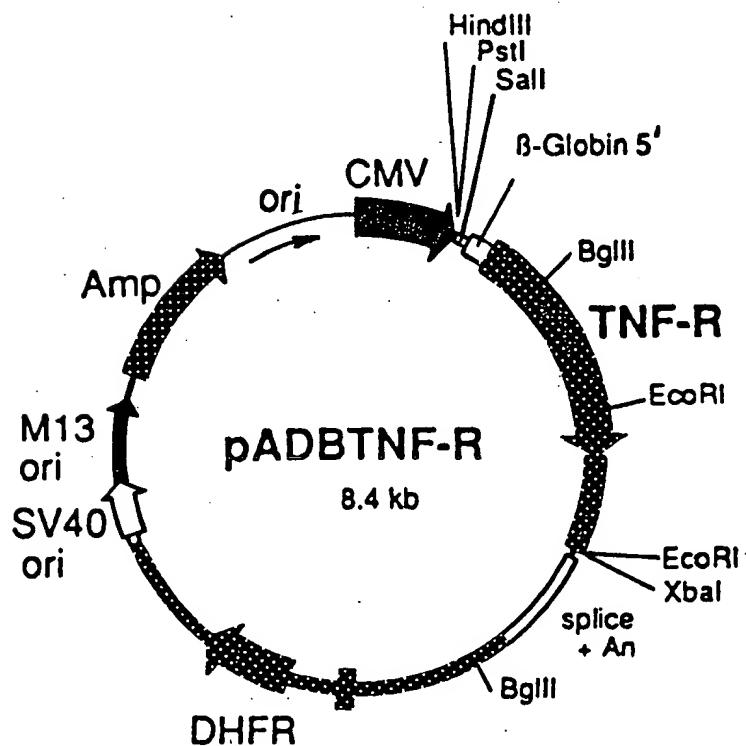


FIG. 8A

raTNF-R

GAATTCCATT TCTCCGAGTT TTCTGAACTC TGGCTCATGA TCGGGCTTAC TGGATACGAG 60
 AATCCTGGAG, GACCGTACCC TGATTTCCAT CTACCTCTGA CTTTGAGCCT TTCTAACCG 120
 GGGCTCACGC TGCCAACACC CGGGCCACCT GGTCGGATCG TCTTACTTCA TTCACCAGCG 180
 TTGCCAATTG CTGCCCTGTC CCCAGCCCCA ATGGGGGAGT GAGAGAGGCC ACTGCCGGCC 240
 GGAC
 245/1 275/11
 ATG GGT CTC CCC ATC GTG CCT GGC CTG CTG TCA CTG GTG CTC CTG GCT CTG CTG ATG
 Met Gly Leu Pro Ile Val Pro Gly Leu Leu Ser Leu Val Leu Leu Ala Leu Leu Met
 305/21 335/31
 GGG ATA CAC CCA TCA GGG GTC ACC GGA CTG GTT CCT TCT CTT GGT GAC CGG GAG AAG AGG
 Gly Ile His Pro Ser Gly Val Thr Gly Leu Val Pro Ser Leu Gly Asp Arg Glu Lys Arg
 365/41 395/51
 GAT AAT TTG TGT CCC CAG GGA AAG TAT GC CAT CCA AAG AAT AAT TCC ATC TGC TGC ACC
 Asp Asn Leu Cys Pro Gln Gly Lys Tyr Ala His Pro Lys Asn Asn Ser Ile Cys Cys Thr
 425/61 455/71
 AAG TGC CAC AAA GGA ACC TAC TTG GTG AGT GAC TGT CCA AGC CCA GGG CAG GAA ACA GTC
 Lys Cys His Lys Gly Thr Tyr Leu Val Ser Asp Cys Pro Ser Pro Gly Gln Glu Thr Val
 485/81 515/91
 TGC GAG CTC TCT CAT AAA GGC ACC TTT ACA GCT TCG CAG AAC CAC GTC AGA CAG TGT CTC
 Cys Glu Leu Ser His Lys Gly Thr Phe Thr Ala Ser Gln Asn His Val Arg Gln Cys Leu
 545/101 575/111
 AGT TGC AAG ACA TGT CGG AAA GAA ATG TTC CAG GTG GAG ATT TCT CCT TGC AAA GCT GAC
 Ser Cys Lys Thr Cys Arg Lys Glu Met Phe Gln Val Glu Ile Ser Pro Cys Lys Ala Asp
 605/121 635/131
 ATG GAC ACC GTG TGT GGC TGC AAG AAC CAA TTC CAG CGC TAC CTG AGT GAG ACG CAT
 Met Asp Thr Val Cys Gly Cys Lys Lys Asn Gln Phe Gln Arg Tyr Leu Ser Glu Thr His
 665/141 695/151
 TTC CAG TGT GTG GAC TGC ACC CCC TGC TTC AAT GGC ACC GTG ACA ATC CCC TGT AAG GAG
 Phe Gln Cys Val Asp Cys Ser Pro Cys Phe Asn Gly Thr Val Thr Ile Pro Cys Lys Glu
 725/161 755/171
 AAA CAG AAC ACC GTG TGT AAC TGC CAC GCA GGA TTC TTT CTA AGC GGA AAT GAG TGC ACC
 Lys Gln Asn Thr Val Cys Asn Cys His Ala Gly Phe Phe Leu Ser Gly Asn Glu Cys Thr
 785/181 815/191
 CCT TGC AGC CAC TGC AAG AAA AAT CAG GAA TGT ATG AAG CTG TGC CTA CCT CCA GTT GCA
 Pro Cys Ser His Cys Lys Asn Gln Glu Cys Met Lys Leu Cys Leu Pro Pro Val Ala
 845/201 875/211
 AAT GTC ACA AAC CCC CAG GAC TCA GGT ACT GCC GTG CTG TTG CCT CTG GTT ATC TTC CTA
 Asn Val Thr Asn Pro Gln Asp Ser Gly Thr Ala Val Leu Leu Pro Leu Val Ile Phe Leu
 905/221 935/231
 GGT CTT TGC CTT TTA TTC TTT ATC TGC ATC AGT CTA CTG TGC CGA TAT CCC CAG TGG AGG
 Gly Leu Cys Leu Leu Phe Phe Ile Cys Ile Ser Leu Leu Cys Arg Tyr Pro Gln Trp Arg
 965/241 995/251
 CCC AGG GTC TAC TCC ATC ATT TGT AGG GAT TCA GCT CCT GTC AAA GAG GTG GAG GGT GAA
 Pro Arg Val Tyr Ser Ile Ile Cys Arg Asp Ser Ala Pro Val Lys Glu Val Glu Gly Glu
 1025/261 1055/271
 GGA ATT GTT ACT AAG CCC CTA ACT CCA GCC TCT ATC CCA GCC TTC AGC CCC AAC CCC GGC
 Gly Ile Val Thr Lys Pro Leu Thr Pro Ala Ser Ile Pro Ala Phe Ser Pro Asn Pro Gly
 1085/281 1115/291
 TTC AAC CCC ACT CTG GGC TTC AGC ACC ACC CCA CGC TTC AGT CAT CCT GTC TCC AGT ACC
 Phe Asn Pro Thr Leu Gly Phe Ser Thr Thr Pro Arg Phe Ser His Pro Val Ser Ser Thr
 1145/301 1175/311
 CCC ATC AGC CCC GTC TTC GGT CCT AGT AAC TGG CAC AAC TTC GTG CCA CCT GTA AGA GAG
 Pro Ile Ser Pro Val Phe Gly Pro Ser Asn Trp His Asn Phe Val Pro Pro Val Arg Glu
 1205/321 1235/331
 GTG GTC CCA ACC CAG GGT GCT GAC CCT CTC CTC TAC GGA TCC CTC AAC CCT GTG CCA ATC
 Val Val Pro Thr Gln Gly Ala Asp Pro Leu Leu Tyr Gly Ser Leu Asn Pro Val Pro Ile

FIG. 8B

1265/341	1295/351
CCC GCC CCT <u>GTT CGG AAA TGG GAA GAC GTC GTC GCG GCC CAG CCA CAA CGG CTT GAC ACT</u>	
Pro Ala Pro Val Arg Lys Trp Glu Asp Val Val Ala Ala Gln Pro Gln Arg Leu Asp Thr	
1325/361	1355/371
GCA GAC CCT GCG ATG CTG TAT GCT GTG GTG GAT GGC GTG CCT CCG ACA CGC TGG AAG GAG	
Ala Asp Pro Ala Met Leu Tyr Ala Val Val Asp Gly Val Pro Pro Thr Arg Trp Lys Glu	
1385/381	1415/391
TTC ATG CGG CTC CTG GGG CTG AGC GAG CAC GAG ATC GAG CGG CTG GAG CTG CAG AAC GGG	
Phe Met Arg Leu Leu Gly Leu Ser Glu His Glu Ile Glu Arg Leu Glu Leu Gln Asn Gly	
1445/401	1475/411
CGT TGC CTC CGC GAG GCT CAT TAC AGC ATG CTG GAA GCC TGG CGG CGC CGC ACA CCG CGA	
Arg Cys Leu Arg Glu Ala His Tyr Ser Met Leu Glu Ala Trp Arg Arg Arg Thr Pro Arg	
1505/421	1535/431
CAC GAG GCC ACG CTG GAC GTA GTG GGC CGC GTG CTT TGC GAC ATG AAC CTG CGT GGC TGC	
His Glu Ala Thr Leu Asp Val Val Gly Arg Val Leu Cys Asp Met Asn Leu Arg Gly Cys	
1565/441	1595/451
CTG GAG AAC ATC CGC GAG ACT CTA GAA AGC CCT GCC CAC TCG TCC ACG ACC CAC CTC CCG	
Leu Glu Asn Ile Arg Glu Thr Leu Glu Ser Pro Ala His Ser Ser Thr Thr His Leu Pro	
1625/461	
CGA TAA	
Arg Stop	
GGCCACACCCC CCACCTCAGG AACGGGACTC GAAGGACCAT CCTGCTAGAT	1680
GCCCTGCTTC CCTGTGAACC TCCTCTTGG TCCTCTAGGG GGCAGGCTCG ATCTGGCAGG	1740
CTCGATCTGG CAGCCACTTC CTTGGTGCTA CCGACTTGGT GTACATAGCT TTTCCCAGCT	1800
GCCGAGGACA GCCTGTGCCA GCCACTTGTG CATGGCAGGG AAGTGTGCCA TCTGCTCCC	1860
GACAGCTGAG GGTGCCAAAA GCCAGGAGAG GTGATTGTGG AGAAAAAGCA CAATCTATCT	1920
GATACCCACT TGGGATGCAA GGACCCAAAC AAAGCTTCTC AGGGCCTCCT CAGTTGATTT	1980
CTGGGCCCTT TTCACAGTAG ATAAAACAGT CTTGTATTG ATTATATCAC ACTAATGGAT	2040
GAACGGTTGA ACTCCCTAAG GTAGGGCAA GCACAGAACAA GTGGGGTCTC CAGCTGGAGC	2100
CCCCGACTCT TGTAATACA CTAAAATCT AAAAGTAAA AAAAAAAA AAAAAAAA	2160
AAAAAAGGAA TTC	

FIG. 9A

huTNF-R

GAATTCTCTG GACTGAGGCT CCAGTTCTGG CCTTTGGGGT TCAAGATCAC TGGGACCAGG 60
 CCGTGATCTC TATGCCCGAG TCTCAACCCT CAACTGTCAC CCCAAGGCAC TTGGGACGTC 120
 CTGGACAGAC CGAGTCCCGG GAAGCCCCAG CACTGCCGCT GCCACACTGC CCTGAGCCCCA 180
 AATGGGGGAG TGAGAGGCCA TAGCTGCTG GC

213/1 243/11
 ATG GGC CTC TCC ACC GTG CCT GAC CTG CTG CCA CTG GTG CTC CTG GAG CTG TTG GTG
 Met Gly Leu Ser Thr Val Pro Asp Leu Leu Leu Pro Leu Val Leu Leu Glu Leu Leu Val
 273/21 303/31
 GGA ATA TAC CCC TCA GGG GTT ATT GGA CTG GTC CCT CAC CTA GGG GAC AGG GAG AAG AGA
 Gly Ile Tyr Pro Ser Gly Val Ile Gly Leu Val Pro His Leu Gly Asp Arg Glu Lys Arg
 333/41 363/51
 GAT AGT GTG TGT CCC CAA GGA AAA TAT ATC CAC CCT CAA AAT AAT TCG ATT TGC TGT ACC
 Asp Ser Val Cys Pro Gln Gly Lys Tyr Ile His Pro Gln Asn Asn Ser Ile Cys Cys Thr
 393/61 423/71
 AAG TGC CAC AAA GGA ACC TAC TTG TAC AAT GAC TGT CCA GGC CCG GGG CAG GAT ACG GAC
 Lys Cys His Lys Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro Gly Gln Asp Thr Asp
 453/81 483/91
 TGC AGG GAG TGT GAG AGC GGC TCC TTC ACC GCT TCA GAA AAC CAC CTC AGA CAC TGC CTC
 Cys Arg Glu Cys Glu Ser Gly Ser Phe Thr Ala Ser Glu Asn His Leu Arg His Cys Leu
 513/101 543/111
 AGC TGC TCC AAA TGC CGA AAG GAA ATG GGT CAG GTG GAG ATC TCT TCT TGC ACA GTG GAC
 Ser Cys Ser Lys Cys Arg Lys Glu Met Gly Gln Val Glu Ile Ser Ser Cys Thr Val Asp
 573/121 603/131
 CGG GAC ACC GTG TGT GGC TGC AGG AAG AAC CAG TAC CGG CAT TAT TGG AGT GAA AAC CTT
 Arg Asp Thr Val Cys Gly Cys Arg Lys Asn Gln Tyr Arg His Tyr Trp Ser Glu Asn Leu
 633/141 663/151
 TTC CAG TGC TTC AAT TGC AGC CTC TGC CTC AAT GGG ACC GTG CAC CTC TCC TGC CAG GAG
 Phe Gln Cys Phe Asn Cys Ser Leu Cys Leu Asn Gly Thr Val His Leu Ser Cys Gln Glu
 693/161 723/171
 AAA CAG AAC ACC GTG TGC ACC TGC CAT GCA GGT TTC TTT CTA AGA GAA AAC GAG TGT GTC
 Lys Gln Asn Thr Val Cys Thr Cys His Ala Gly Phe Phe Leu Arg Glu Asn Glu Cys Val
 753/181 783/191
 TCC TGT AGT AAC TGT AAG AAA AGC CTG GAG TGC ACG AAG TTG TGC CTA CCC CAG ATT GAG
 Ser Cys Ser Asn Cys Lys Ser Leu Glu Cys Thr Lys Leu Cys Leu Pro Gln Ile Glu
 813/201 843/211
 AAT GTT AAG GGC ACT GAG GAC TCA GGC ACC ACA GTG CTG TTG CCC CTG GTC ATT TTC TTT
 Asn Val Lys Gly Thr Glu Asp Ser Gly Thr Thr Val Leu Leu Pro Leu Val Ile Phe Phe
 873/221 903/231
 GGT CTT TGC CTT TTA TCC CTC CTC TTC ATT GGT TTA ATG TAT CGC TAC CAA CGG TGG AAG
 Gly Leu Cys Leu Leu Ser Leu Phe Ile Gly Leu Met Tyr Arg Tyr Gln Arg Trp Lys
 933/241 963/251
 TCC AAG CTC TAC TCC ATT GTT TGT GGG AAA TCG ACA CCT GAA AAA GAG GGG GAG CTT GAA
 Ser Lys Leu Tyr Ser Ile Val Cys Gly Lys Ser Thr Pro Glu Lys Glu Gly Leu Glu
 993/261 1023/271
 GGA ACT ACT ACT AAG CCC CTG GCC CCA AAC CCA AGC TTC AGT CCC ACT CCA GGC TTC ACC
 Gly Thr Thr Thr Lys Pro Leu Ala Pro Asn Pro Ser Phe Ser Pro Thr Pro Gly Phe Thr
 1053/281 1083/291
 CCC ACC CTG GGC TTC AGT CCC GTG CCC AGT TCC ACC TTC ACC TCC AGC TCC ACC TAT ACC
 Pro Thr Leu Gly Phe Ser Pro Val Pro Ser Ser Thr Phe Thr Ser Ser Ser Thr Tyr Thr
 1113/301 1143/311
 CCC GGT GAC TGT CCC AAC TTT GCG GCT CCC CGC AGA GAG GTG GCA CCA CCC TAT CAG GGG
 Pro Gly Asp Cys Pro Asn Phe Ala Ala Pro Arg Arg Glu Val Ala Pro Pro Tyr Gln Gly
 1173/321 1203/331
 GCT GAC CCC ATC CTT GCG ACA GCC CTC GCC TCC GAC CCC ATC CCC AAC CCC CTT CAG AAG
 Ala Asp Pro Ile Leu Ala Thr Ala Leu Ala Ser Asp Pro Ile Pro Asn Pro Leu Gln Lys

FIG. 9B

1233/341	1263/351
TGG GAG GAC AGC GCC CAC AAG CCA CAG AGC CTA GAC ACT GAT GAC CCC GCG ACG CTG TAC	
Trp Glu Asp Ser Ala His Lys Pro Gln Ser Leu Asp Thr Asp Asp Pro Ala Thr Leu Tyr	
1293/361	1323/371
GCC GTG GTG GAG AAC GTG CCC CCG TTG CGC TGG AAG GAA TTC GTG CGG CGC CTA GGG CTG	
Ala Val Val Glu Asn Val Pro Pro Leu Arg Trp Lys Glu Phe Val Arg Arg Leu Gly Leu	
1353/381	1383/391
AGC GAC CAC GAG ATC GAT CGG CTG GAG CTG CAG AAC GGG CGC TGC CTG CGC GAG GCG CAA	
Ser Asp His Glu Ile Asp Arg Leu Glu Leu Gln Asn Gly Arg Cys Leu Arg Glu Ala Gln	
1413/401	1443/411
TAC AGC ATG CTG GCG ACC TGG AGG CGG CGC ACG CCG CGG CGC GAG GCC ACG CTG GAG CTG	
Tyr Ser Met Leu Ala Thr Trp Arg Arg Arg Thr Pro Arg Arg Glu Ala Thr Leu Glu Leu	
1473/421	1503/431
CTG GGA CGC GTG CTC CGC GAC ATG GAC CTG CTG GGC TGC CTG GAG GAC ATC GAG GAG GCG	
Leu Gly Arg Val Leu Arg Asp Met Asp Leu Leu Gly Cys Leu Glu Asp Ile Glu Glu Ala	
1533/441	1563/451
CTT TGC GGC CCC GCC CTC CCG CCC GCG CCC AGT CTT CTC AGA TGA	1580
Leu Cys Gly Pro Ala Ala Leu Pro Pro Ala Pro Ser Leu Leu Arg Stop	
GGCTGCGCCC CTGCGGGCAG CTCTAAGGAC CGTCCTGCGA	1620
GATCGCCTTC CAACCCCCACT TTTTCTGGA AAGGAGGGGT CCTGCAGGGG CAAGCAGGAG	1680
CTAGCAGCCG CCTACTTGTT GCTAACCCCT CGATGTACAT AGCTTTCTC AGCTGCCTGC	1740
GCGCCGCCGA CAGTCAGCGC TGTGCGCGCG GAGAGAGGTG CGCCGTGGGC TCAAGAGCCT	1800
GAGTGGGTGG TTTGCGAGGA TGAGGGACGC TATGCCCTCAT GCCCCTTTG GGTGTCCCTCA	1860
CCAGCAAGGC TGCTCGGGGG CCCCTGGTTC GTCCCTGAGC CTTTTTCACA GTGCATAAGC	1920
AGTTTTTTT GTTTTGT TT TGTTTGT TT TGTTTTAAA TCAATCATGT TACACTAATA	1980
GAAACTTGGC ACTCCTGTGC CCTCTGCCCTG GACAAGCACA TAGCAAGCTG AACTGTCCCTA	2040
AGGCAGGGGC GAGCACGGAA CAATGGGGCC TTCAGCTGGA GCTGTGGACT TTTGTACATA	2100
CACTAAAATT CTGAAGTTAA AAAAAAAA AAAAGGAATT C	2141

FIG.10

